

Query= SEQ ID NO:1
(2772 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL365232.24.1.120846	<u>1913</u>	0.0
AL445569.1.1.47057	<u>733</u>	0.0
AL360236.26.1.154998	<u>355</u>	1e-94

>AL365232.24.1.120846
Length = 120846

Score = 1913 bits (965), Expect = 0.0
Identities = 965/965 (100%)
Strand = Plus / Plus

Query: 1808 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacagggtccttc 1867
|||||
Sbjct: 61339 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacagggtccttc 61398

Query: 1868 ggaaaggctctgcctcagccctcgctttggcttcattccagatcccaccttttgaatgtg 1927
|||||
Sbjct: 61399 ggaaaggctctgcctcagccctcgctttggcttcattccagatcccaccttttgaatgtg 61458

Query: 1928 aacagacatctgactatcaaagccctgtggatagcaaagatctttcgggttccgcacaaa 1987
|||||
Sbjct: 61459 aacagacatctgactatcaaagccctgtggatagcaaagatctttcgggttccgcacaaa 61518

Query: 1988 acagtggctgcttatccagatcaactagtgcacaacatctcgagaggcctgcagttcattc 2047
|||||
Sbjct: 61519 acagtggctgcttatccagatcaactagtgcacaacatctcgagaggcctgcagttcattc 61578

Query: 2048 tgacgccaaatgagttcagtgcccagactttctacgcgcttagccctactatgcacagtc 2107
|||||
Sbjct: 61579 tgacgccaaatgagttcagtgcccagactttctacgcgcttagccctactatgcacagtc 61638

Query: 2108 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtgccagccaccaacacca 2167
|||||
Sbjct: 61639 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtgccagccaccaacacca 61698

Query: 2168 ttgcaaaccaaataaatacggcacccaagccagcagccccaacaactttacagatccac 2227
|||||
Sbjct: 61699 ttgcaaaccaaataaatacggcacccaagccagcagccccaacaactttacagatccac 61758

Query: 2228 ctctctctccagccatcaagcatctgccaggccagaaactctgcaccctaaccctgcag 2287
|||||
Sbjct: 61759 ctctctctccagccatcaagcatctgccaggccagaaactctgcaccctaaccctgcag 61818

Query: 2288 gcttacaggaaagcatttctgacgtcaccacctgccttggtgcctccaaggaaaatgttc 2347
|||||
Sbjct: 61819 gcttacaggaaagcatttctgacgtcaccacctgccttggtgcctccaaggaaaatgttc 61878

Query: 2348 aggttgcacagtcaaatctcaccaaggaccgttctatgaggaaaagctttgacatgggag 2407
|||||
Sbjct: 61879 aggttgcacagtcaaatctcaccaaggaccgttctatgaggaaaagctttgacatgggag 61938

Query: 2408 gagaaactctgttgtctgtctgtcccatggtgccgaaggacttgggcaaatctttgtctg 2467
|||||
Sbjct: 61939 gagaaactctgttgtctgtctgtcccatggtgccgaaggacttgggcaaatctttgtctg 61998

Query: 2468 tgcaaaacctgatcaggtcgaccgaggaactgaatatacaactttcagggagtgagtcaa 2527
|||||
Sbjct: 61999 tgcaaaacctgatcaggtcgaccgaggaactgaatatacaactttcagggagtgagtcaa 62058

Query: 2528 gtggctccagaggcagccaagatttttaccctaaatggaggggaatccaaattgtttataa 2587
|||||
Sbjct: 62059 gtggctccagaggcagccaagatttttaccctaaatggaggggaatccaaattgtttataa 62118

Query: 2588 ctgatgaagaggtgggtcccgaagagacagagacagacacttttgatgccgcaccgcagc 2647
|||||
Sbjct: 62119 ctgatgaagaggtgggtcccgaagagacagagacagacacttttgatgccgcaccgcagc 62178

Query: 2648 ctgccaggaagctgcctttgcatcagactctctaaggactggaaggtcacgatcatctc 2707
|||||
Sbjct: 62179 ctgccaggaagctgcctttgcatcagactctctaaggactggaaggtcacgatcatctc 62238

Query: 2708 agagcatttgaaggcaggagaaagtacagatgccctcagcttgccctcatgtcaaaactga 2767
|||||
Sbjct: 62239 agagcatttgaaggcaggagaaagtacagatgccctcagcttgccctcatgtcaaaactga 62298

Query: 2768 aataa 2772
|||||
Sbjct: 62299 aataa 62303

Score = 438 bits (221), Expect = e-120
Identities = 221/221 (100%)
Strand = Plus / Plus

Query: 1221 tcagaagctaagttttaaggagcgagtgcgcatggctagccccaggggccagagtattaa 1280
|||||
Sbjct: 310 tcagaagctaagttttaaggagcgagtgcgcatggctagccccaggggccagagtattaa 369

Query: 1281 gagccgacaagcctcagtaggtgacaggaggtccccaagcaccgacatcacagccgaggg 1340
|||||
Sbjct: 370 gagccgacaagcctcagtaggtgacaggaggtccccaagcaccgacatcacagccgaggg 429

Query: 1341 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 1400
|||||
Sbjct: 430 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 489

Query: 1401 gctgcgctcaaaagttctcagccaaaaccagtgatagatg 1441
|||||
Sbjct: 490 gctgcgctcaaaagttctcagccaaaaccagtgatagatg 530

Score = 268 bits (135), Expect = 2e-68
Identities = 135/135 (100%)
Strand = Plus / Plus

Query: 1548 cagaattatgaaatttcatgttgcaaaacggaagttaaggaaacattacgtccatatga 1607
|||||
Sbjct: 57459 cagaattatgaaatttcatgttgcaaaacggaagttaaggaaacattacgtccatatga 57518

Query: 1608 tgtaaaagatgtcattgaacaatattctgctggtcatctggacatgttggtgtagaattaa 1667
|||||
Sbjct: 57519 tgtaaaagatgtcattgaacaatattctgctggtcatctggacatgttggtgtagaattaa 57578

Query: 1668 aagccttcaaacacg 1682
|||||
Sbjct: 57579 aagccttcaaacacg 57593

Score = 264 bits (133), Expect = 3e-67
Identities = 133/133 (100%)
Strand = Plus / Plus

Query: 1682 gtgttgatcaaattcttgaaaagggcaaatacacatcagataagaagagccgagagaaaa 1741
|||||
Sbjct: 59453 gtgttgatcaaattcttgaaaagggcaaatacacatcagataagaagagccgagagaaaa 59512

Query: 1742 taacagcagaacatgagaccacagacgatctcagtatgctcggtcgggtgggtcaagggtg 1801
|||||
Sbjct: 59513 taacagcagaacatgagaccacagacgatctcagtatgctcggtcgggtgggtcaagggtg 59572

Query: 1802 aaaaacaggtaca 1814
|||||
Sbjct: 59573 aaaaacaggtaca 59585

Score = 218 bits (110), Expect = 1e-53
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1441 gctgacacagcccttggcactgatgatgtatatgatgaaaaggatgccagtgtgatgta 1500
|||||
Sbjct: 36634 gctgacacagcccttggcactgatgatgtatatgatgaaaaggatgccagtgtgatgta 36693

Query: 1501 tcagtggaagacctcaccaccacttaaaactgtcattcgagctatcag 1550
|||||
Sbjct: 36694 tcagtggaagacctcaccaccacttaaaactgtcattcgagctatcag 36743

>AL445569.1.1.47057
Length = 47057

Score = 733 bits (370), Expect = 0.0
Identities = 394/401 (98%), Gaps = 6/401 (1%)
Strand = Plus / Plus

Query: 1 atgccccgccaccacgcgggaggagaggagggcgccgcccgggctctgggtgaagagc 60
|||||
Sbjct: 4316 atgccccgccaccacgcgggaggagaggagggcgccgcccgggctctgggtgaagagc 4375

Query: 61 ggcgagcggcgggcgggcgggcgggggcgcttgggcagcgccatgaaggatgtggag 120
|||||
Sbjct: 4376 ggcgagcggcgggcgggcgggcgggggcgcttgggcagcgccatgaaggatgtggag 4435

Query: 121 tcgggccggggcaggggtgctgctgaactcggcagccgccagggcgacggcctgctactg 180
|||||
Sbjct: 4436 tcgggccggggcaggggtgctgctgaactcggcagccgccagggcgacggcctgctactg 4495

Query: 181 ctgggcacccgcgcggccacgctcggtggcgggcggtggcctgagggagagccgccgg 240
|||||
Sbjct: 4496 ctgggcacccgcgcggccacgctcggtggcgggcggtggcctgagggagagccgccgg 4555

Query: 241 ggcaagcagggggcccggatgagcctgctggggaagccgctctcttacacgagtagccag 300
|||||
Sbjct: 4556 ggcaagcagggggcccggatgagcctgctggggaagccgctctcttacacgagtagccag 4615

Query: 301 agctgccggcgcaacgtcaagtaccggcggggtgcagaactacctgtacaacgtgctggag 360
|||||
Sbjct: 4616 agctgccggcgcaacgtcaagtaccggcggggtgcagaactacctgtacaacgtgctggag 4675

Query: 361 agaccccgcggtgggcttcatctaccacgctttcgt 398
|||||
Sbjct: 4676 agaccccgcggtgggcttcatctaccacgctttcgt 4713

>AL360236.26.1.154998
Length = 154998

Score = 355 bits (179), Expect = 1e-94
Identities = 179/179 (100%)
Strand = Plus / Plus

Query: 615 agataccattgttcttatcgcttcaatagcagttgtttctgcaaaaactcagggtaatat 674
|||||
Sbjct: 99107 agataccattgttcttatcgcttcaatagcagttgtttctgcaaaaactcagggtaatat 99166

Query: 675 ttttgccacgtctgcactcagaagtctccgtttcctacagatcctccgcatgggtgcgcat 734
|||||
Sbjct: 99167 ttttgccacgtctgcactcagaagtctccgtttcctacagatcctccgcatgggtgcgcat 99226

Query: 735 ggaccgaaggggaggcacttggaaattactgggttcagtgggtttatgctcacagcaagg 793
|||||
Sbjct: 99227 ggaccgaaggggaggcacttggaaattactgggttcagtgggtttatgctcacagcaagg 99285

Score = 254 bits (128), Expect = 3e-64
Identities = 128/128 (100%)
Strand = Plus / Plus

Query: 489 ggagttcgtgatgattgtcgtctttggtttgagttcatcattcgaatctggtctgcggg 548
|||||
Sbjct: 63722 ggagttcgtgatgattgtcgtctttggtttgagttcatcattcgaatctggtctgcggg 63781

Query: 549 ttgctgttgctcgatatagaggatggcaaggaagactgaggtttgctcgaaagcccttctg 608
|||||
Sbjct: 63782 ttgctgttgctcgatatagaggatggcaaggaagactgaggtttgctcgaaagcccttctg 63841

Query: 609 tgttatag 616
|||||
Sbjct: 63842 tgttatag 63849

Score = 254 bits (128), Expect = 3e-64
Identities = 128/128 (100%)
Strand = Plus / Plus

Query: 791 aggaattaatcacagcttggtacataggatttttggttcttattttttcgtctttccttg 850
|||||
Sbjct: 99547 aggaattaatcacagcttggtacataggatttttggttcttattttttcgtctttccttg 99606

Query: 851 tctatctggtggaaaaggatgccaataaagagttttctacatatgcagatgctctctggt 910
|||||
Sbjct: 99607 tctatctggtggaaaaggatgccaataaagagttttctacatatgcagatgctctctggt 99666

Query: 911 ggggcaca 918
|||||
Sbjct: 99667 ggggcaca 99674

Score = 222 bits (112), Expect = 9e-55
Identities = 112/112 (100%)
Strand = Plus / Plus

Query: 919 attacattgacaactattggctatggagacaaaactcccctaacttggtgggaagattg 978
|||||
Sbjct: 127044 attacattgacaactattggctatggagacaaaactcccctaacttggtgggaagattg 127103

Query: 979 ctttctgcaggctttgcactccttggcatttctttctttgcacttctgccc 1030
|||||
Sbjct: 127104 ctttctgcaggctttgcactccttggcatttctttctttgcacttctgccc 127155

Score = 194 bits (98), Expect = 2e-46
Identities = 98/98 (100%)
Strand = Plus / Plus

Query: 1123 cagtgtgtttggcgtagttacgcagctgatgagaaatctgtttccattgcaacctggaag 1182
|||||
Sbjct: 142267 cagtgtgtttggcgtagttacgcagctgatgagaaatctgtttccattgcaacctggaag 142326

Query: 1183 ccacacttgaaggccttgcacacctgcagccctaccaa 1220
|||||
Sbjct: 142327 ccacacttgaaggccttgcacacctgcagccctaccaa 142364

Score = 190 bits (96), Expect = 3e-45
Identities = 96/96 (100%)
Strand = Plus / Plus

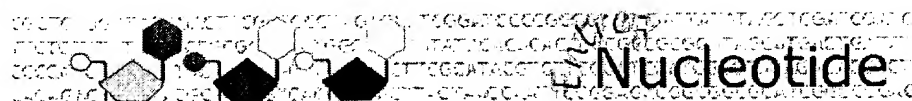
Query: 1030 ggcattcttggctcagggttttgcattaaaagtacaagaacaacaccgccagaaacattt 1089
|||||
Sbjct: 133095 ggcattcttggctcagggttttgcattaaaagtacaagaacaacaccgccagaaacattt 133154

Query: 1090 gagaaaagaaggaacccagctgccaacctcattcag 1125
|||||
Sbjct: 133155 gagaaaagaaggaacccagctgccaacctcattcag 133190

Score = 182 bits (92), Expect = 8e-43
Identities = 92/92 (100%)
Strand = Plus / Plus

Query: 399 ttttctccttgtctttggttgcttgattttgtcagtgttttctaccatccctgagcacac 458
 ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 25695 ttttctccttgtctttggttgcttgattttgtcagtgttttctaccatccctgagcacac 25754

Query: 459 aaaattggcctcaagttgcctcttgatcctgg 490
 ||||||||||||||||||||
Sbjct: 25755 aaaattggcctcaagttgcctcttgatcctgg 25786



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LOCUS AL365232 120846 bp DNA linear PRI 01-MAR-2001

DEFINITION Human DNA sequence from clone RP11-257K9 on chromosome 6, complete sequence.

ACCESSION AL365232

VERSION AL365232.24 GI:13234949

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 120846)

AUTHORS Williams, S.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Mar 5, 2001 this sequence version replaced [gi:13160293](#). During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>

RP11-257K9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-257K9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-257K9 is at 1 in this sequence. The



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Features

1: [AL445569](#). Human DNA sequenc...[gi:10862812]

Links

LOCUS AL445569 47057 bp DNA linear PRI 17-OCT-2000

DEFINITION Human DNA sequence from clone RP11-135M8 on chromosome 6, complete sequence.

ACCESSION AL445569 AL161434

VERSION AL445569.1 GI:10862812

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 47057)

AUTHORS Bates, K.

TITLE Direct Submission

JOURNAL Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>

RP11-135M8 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-135M8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-474G15 is at 100 in this sequence.

The true right end of clone RP11-135M8 is at 47057 in this sequence.



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1: AL360236. Human DNA sequenc...[gi:13398790]

Links

LOCUS AL360236 154998 bp DNA linear PRI 19-MAR-2001

DEFINITION Human DNA sequence from clone RP11-380M3 on chromosome 6, complete sequence.

ACCESSION AL360236

VERSION AL360236.26 GI:13398790

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 154998)

AUTHORS Clark,G.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Mar 21, 2001 this sequence version replaced gi:13161652. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-380M3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-380M3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-380M3 is at 1 in this sequence. The